

SCORE Search Results Details for Application 10539637  
and Search Result 20070420\_155801\_us-10-539-637-  
1.rag.

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This page gives you Search Results detail for the Application 10539637 and Search Result 20070420\_155801\_us-10-539-637-1.rag.

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OM protein - protein search, using sw model

Run on: April 21, 2007, 06:24:28 ; Search time 245 Seconds  
(without alignments)  
251.370 Million cell updates/sec

Title: US-10-539-637-1  
Perfect score: 54  
Sequence: 1 CXXXXXXXXXXXXXXXXXXXXX.....XXXXXXXXXXXXXXXXXXXXX 126

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2782304 seqs, 489333398 residues

Total number of hits satisfying chosen parameters: 2782304

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_200701:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*  
9: geneseqp2005s:\*  
10: geneseqp2006s:\*  
11: geneseqp2007s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		Query			Description
No.	Score	Match	Length	ID	

1	24	44.4	969	10	AEI58969	Aei58969 Soybean p
2	22	40.7	1298	10	AEI58307	Aei58307 Thale cre
3	22	40.7	1363	10	AEI55891	Aei55891 Thale cre
4	22	40.7	1363	10	AEI57963	Aei57963 Thale cre
5	22	40.7	1484	10	AEI55957	Aei55957 Thale cre
6	19	35.2	5304	8	ADP30706	Adp30706 Human sec
7	19	35.2	6465	8	ADP30705	Adp30705 Human sec
8	18	33.3	720	10	AEI60499	Aei60499 Zea mays
9	18	33.3	813	10	AEI58279	Aei58279 Thale cre
10	18	33.3	997	10	AEI59937	Aei59937 Soybean p
11	18	33.3	1066	10	AEI56935	Aei56935 Thale cre
12	18	33.3	1098	10	AEI57947	Aei57947 Thale cre
13	18	33.3	1099	10	AEI55933	Aei55933 Thale cre
14	18	33.3	1270	10	AEI56785	Aei56785 Zea mays
15	18	33.3	1337	10	AEI55837	Aei55837 Thale cre
16	18	33.3	1340	10	AEI57945	Aei57945 Thale cre
17	18	33.3	1592	10	AEI60621	Aei60621 Soybean p
18	18	33.3	1593	10	AEK75211	Aek75211 Human KIR
19	18	33.3	1825	10	AEI56415	Aei56415 Zea mays
20	18	33.3	2073	10	AEI58211	Aei58211 Thale cre
21	17	31.5	266	7	ABO74515	Abo74515 Pseudomon
22	17	31.5	1090	8	ADQ10187	Adq10187 Human pol
23	17	31.5	1129	10	AEI55865	Aei55865 Thale cre
24	17	31.5	1289	8	ADP30675	Adp30675 Human sec
25	17	31.5	1289	10	AEI55967	Aei55967 Thale cre
26	17	31.5	1315	10	AEI59781	Aei59781 Bread whe
27	17	31.5	1336	10	AEI56065	Aei56065 Zea mays
28	17	31.5	1338	10	AEI58073	Aei58073 Thale cre
29	17	31.5	1339	10	AEI55961	Aei55961 Thale cre
30	17	31.5	1348	10	AEI57985	Aei57985 Thale cre
31	17	31.5	1396	10	AEI55999	Aei55999 Thale cre
32	17	31.5	1440	8	ADG34533	Adg34533 Glucocort
33	17	31.5	1461	10	AEI58357	Aei58357 Thale cre
34	17	31.5	1469	10	AEI56989	Aei56989 Thale cre
35	17	31.5	1486	10	AEI58055	Aei58055 Thale cre
36	17	31.5	1660	10	AEI57665	Aei57665 Thale cre
37	17	31.5	1661	10	AEI57325	Aei57325 Thale cre
38	17	31.5	1693	10	AEI59723	Aei59723 Soybean p
39	17	31.5	1703	10	AEI57913	Aei57913 Thale cre
40	17	31.5	1713	10	AEI57285	Aei57285 Thale cre
41	17	31.5	1744	10	AEI58283	Aei58283 Thale cre
42	17	31.5	1851	10	AEI57773	Aei57773 Thale cre
43	17	31.5	1860	10	AEI59665	Aei59665 Zea mays
44	17	31.5	1945	10	AEI57505	Aei57505 Thale cre
45	17	31.5	2097	10	AEI59677	Aei59677 Zea mays

ALIGNMENTS

RESULT 1  
AEI58969  
ID AEI58969 standard; protein; 969 AA.  
XX  
AC AEI58969;  
XX  
DT 24-AUG-2006 (first entry)  
XX  
DE Soybean polypeptide, SEQ ID NO: 3436.  
XX  
KW plant; transgenic plant; mapping.  
XX  
OS Glycine max.  
XX

SCORE Search Results Details for Application 10539637  
and Search Result 20070420\_155801\_us-10-539-637-  
2.rag.

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OM protein - protein search, using sw model

Run on: April 21, 2007, 06:24:28 ; Search time 128 Seconds  
(without alignments)  
251.370 Million cell updates/sec

Title: US-10-539-637-2  
Perfect score: 54  
Sequence: 1 CXXXXXXXXXXCXXXXXXXXX.....XXXXXXXXXXCXXXXXXXXXX 66

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2782304 seqs, 489333398 residues

Total number of hits satisfying chosen parameters: 2782304

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_200701:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*  
9: geneseqp2005s:\*  
10: geneseqp2006s:\*  
11: geneseqp2007s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		Query			Description
No.	Score	Match	Length	ID	

1	35	64.8	1092	10	AEI57599	Aei57599 Thale cre
2	35	64.8	1175	10	AEI58821	Aei58821 Bread whe
3	34	63.0	1044	8	ADP31517	Adp31517 Human sec
4	33	61.1	1073	10	AEI56845	Aei56845 Thale cre
5	33	61.1	1617	8	ADP30660	Adp30660 Human sec
6	32	59.3	642	8	ADP31161	Adp31161 Human sec
7	32	59.3	938	10	AEI56329	Aei56329 Zea mays
8	32	59.3	1944	10	AEI57975	Aei57975 Thale cre
9	31	57.4	785	10	AEI58535	Aei58535 Soybean p
10	31	57.4	813	8	ADP30649	Adp30649 Human sec
11	31	57.4	976	10	AEI57003	Aei57003 Thale cre
12	31	57.4	1355	10	AEI57811	Aei57811 Thale cre
13	31	57.4	1395	10	AEI56663	Aei56663 Zea mays
14	31	57.4	1863	10	AEI56521	Aei56521 Zea mays
15	31	57.4	7285	6	ABJ38280	Abj38280 pAMG21-RA
16	30	55.6	1568	10	AEI58079	Aei58079 Thale cre
17	30	55.6	1595	10	AEI57633	Aei57633 Thale cre
18	30	55.6	1732	10	AEI58365	Aei58365 Thale cre
19	30	55.6	1785	10	AEI58277	Aei58277 Thale cre
20	30	55.6	2068	10	AEI58195	Aei58195 Thale cre
21	30	55.6	2077	10	AEI55857	Aei55857 Thale cre
22	30	55.6	2643	10	AEI57397	Aei57397 Thale cre
23	29.5	54.6	1050	8	ADP31370	Adp31370 Human sec
24	29.5	54.6	3658	10	AEI57201	Aei57201 Thale cre
25	29	53.7	279	8	ADP30846	Adp30846 Human sec
26	29	53.7	279	8	ADP30844	Adp30844 Human sec
27	29	53.7	929	10	AEI58829	Aei58829 Zea mays
28	29	53.7	1176	10	AEI55601	Aei55601 Thale cre
29	29	53.7	1220	10	AEI57075	Aei57075 Thale cre
30	29	53.7	1642	10	AEI56957	Aei56957 Thale cre
31	29	53.7	1766	10	AEI58147	Aei58147 Thale cre
32	29	53.7	1801	10	AEI58193	Aei58193 Thale cre
33	29	53.7	1848	8	ADP31372	Adp31372 Human sec
34	29	53.7	1880	10	AEI57635	Aei57635 Thale cre
35	29	53.7	2110	10	AEI57543	Aei57543 Thale cre
36	29	53.7	2175	10	AEI57541	Aei57541 Thale cre
37	29	53.7	2445	10	AEI57585	Aei57585 Thale cre
38	28.5	52.8	1614	8	ADP31529	Adp31529 Human sec
39	28	51.9	899	10	AEI56797	Aei56797 Thale cre
40	28	51.9	1026	10	AEI57051	Aei57051 Thale cre
41	28	51.9	1075	10	AEI56363	Aei56363 Thale cre
42	28	51.9	1146	10	AEI55617	Aei55617 Thale cre
43	28	51.9	1272	10	AEI57239	Aei57239 Thale cre
44	28	51.9	1412	10	AEI58605	Aei58605 Bread whe
45	28	51.9	1417	10	AEI58029	Aei58029 Thale cre

## ALIGNMENTS

## RESULT 1

AEI57599

ID AEI57599 standard; protein; 1092 AA.

XX

AC AEI57599;

XX

DT 24-AUG-2006 (first entry)

XX

DE Thale cress polypeptide, SEQ ID NO: 2066.

XX

KW plant; transgenic plant; mapping.

XX

OS Arabidopsis thaliana.

XX

SCORE Search Results Details for Application 10539637  
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3.rag.

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OM protein - protein search, using sw model

Run on: April 21, 2007, 06:24:28 ; Search time 82 Seconds  
(without alignments)  
251.370 Million cell updates/sec

Title: US-10-539-637-3  
Perfect score: 54  
Sequence: 1 CXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX 42

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2782304 seqs, 489333398 residues

Total number of hits satisfying chosen parameters: 2782304

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_200701:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*  
9: geneseqp2005s:\*  
10: geneseqp2006s:\*  
11: geneseqp2007s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%			
Result	Query				
No.	Score	Match	Length	ID	Description

1	47	87.0	1049	10	AEI56157	Aei56157 Zea mays
2	47	87.0	1744	10	AEI56113	Aei56113 Zea mays
3	46	85.2	1408	10	AEI55995	Aei55995 Thale cre
4	45	83.3	1116	8	ADP31692	Adp31692 Human sec
5	45	83.3	1415	10	AEI57295	Aei57295 Thale cre
6	45	83.3	1479	10	AEI57893	Aei57893 Thale cre
7	45	83.3	1719	10	AEI57393	Aei57393 Thale cre
8	45	83.3	2008	10	AEI57193	Aei57193 Thale cre
9	44	81.5	1077	10	AEI57163	Aei57163 Thale cre
10	44	81.5	1388	10	AEI56799	Aei56799 Thale cre
11	44	81.5	1478	10	AEI56975	Aei56975 Thale cre
12	44	81.5	1693	10	AEI59723	Aei59723 Soybean p
13	43	79.6	353	8	ADP31558	Adp31558 Human sec
14	43	79.6	948	8	ADP30586	Adp30586 Human sec
15	43	79.6	1456	10	AEI56697	Aei56697 Zea mays
16	43	79.6	1730	10	AEI57821	Aei57821 Thale cre
17	43	79.6	4752	8	ADP30585	Adp30585 Human sec
18	43	79.6	4752	8	ADP30651	Adp30651 Human sec
19	42	77.8	185	8	ADP31109	Adp31109 Human sec
20	42	77.8	1172	10	AEI55885	Aei55885 Thale cre
21	42	77.8	1172	10	AEI57949	Aei57949 Thale cre
22	42	77.8	1345	10	AEI58105	Aei58105 Thale cre
23	42	77.8	1348	10	AEI55887	Aei55887 Thale cre
24	42	77.8	1435	10	AEI60567	Aei60567 Soybean p
25	42	77.8	1492	10	AEI58447	Aei58447 Soybean p
26	42	77.8	1538	10	AEI57907	Aei57907 Thale cre
27	42	77.8	1712	10	AEI56619	Aei56619 Zea mays
28	42	77.8	1714	10	AEI56273	Aei56273 Zea mays
29	42	77.8	1972	10	AEI58271	Aei58271 Thale cre
30	42	77.8	2056	10	AEI58355	Aei58355 Thale cre
31	42	77.8	2073	10	AEI58211	Aei58211 Thale cre
32	42	77.8	2411	10	AEI60151	Aei60151 Soybean p
33	41	75.9	369	8	ADP31047	Adp31047 Human sec
34	41	75.9	533	8	ADP31279	Adp31279 Human sec
35	41	75.9	711	8	ADP31440	Adp31440 Human sec
36	41	75.9	960	8	ADP31471	Adp31471 Human sec
37	41	75.9	960	8	ADP31470	Adp31470 Human sec
38	41	75.9	1092	8	ADP31358	Adp31358 Human sec
39	41	75.9	1110	8	ADP31430	Adp31430 Human sec
40	41	75.9	1179	8	ADP30486	Adp30486 Human sec
41	41	75.9	1258	10	AEI57145	Aei57145 Thale cre
42	41	75.9	1392	10	AEI59283	Aei59283 Bread whe
43	41	75.9	1398	8	ADP31488	Adp31488 Human sec
44	41	75.9	1782	8	ADP31270	Adp31270 Human sec
45	41	75.9	2187	8	ADP30882	Adp30882 Human sec

#### ALIGNMENTS

#### RESULT 1

AEI56157

ID AEI56157 standard; protein; 1049 AA.

XX

AC AEI56157;

XX

DT 24-AUG-2006 (first entry)

XX

DE Zea mays polypeptide, SEQ ID NO: 624.

XX

KW plant; transgenic plant; mapping.

XX

OS Zea mays.

XX

SCORE Search Results Details for Application 10539637  
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4.rag.

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OM protein - protein search, using sw model

Run on: April 21, 2007, 06:24:28 ; Search time 64 Seconds  
(without alignments)  
251.370 Million cell updates/sec

Title: US-10-539-637-4  
Perfect score: 54  
Sequence: 1 CXXXCXXXCXXXXXXXXCXCCCCCXXXXXXXX 33

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2782304 seqs, 489333398 residues

Total number of hits satisfying chosen parameters: 2782304

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_200701:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*  
9: geneseqp2005s:\*  
10: geneseqp2006s:\*  
11: geneseqp2007s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		Query				Description
No.	Score	Match	Length	DB	ID	

1	51	94.4	1663	10	AEI56561	Aei56561 Thale cre
2	50	92.6	1173	10	AEI57787	Aei57787 Thale cre
3	50	92.6	1524	10	AEI56419	Aei56419 Zea mays
4	50	92.6	1867	10	AEI55939	Aei55939 Thale cre
5	50	92.6	1867	10	AEI58137	Aei58137 Thale cre
6	49	90.7	1152	10	AEI58245	Aei58245 Thale cre
7	49	90.7	1192	10	AEI58347	Aei58347 Thale cre
8	49	90.7	1206	10	AEI56449	Aei56449 Thale cre
9	49	90.7	1296	10	AEI57613	Aei57613 Thale cre
10	49	90.7	2682	10	AEI55621	Aei55621 Thale cre
11	48	88.9	699	10	AEI57133	Aei57133 Thale cre
12	48	88.9	849	8	ADP31184	Adp31184 Human sec
13	48	88.9	1143	10	AEI56025	Aei56025 Thale cre
14	48	88.9	1424	10	AEI58075	Aei58075 Thale cre
15	47	87.0	1221	10	AEI57205	Aei57205 Thale cre
16	47	87.0	1281	10	AEI57359	Aei57359 Thale cre
17	47	87.0	1572	10	AEI57493	Aei57493 Thale cre
18	47	87.0	1951	10	AEI58651	Aei58651 Soybean p
19	46	85.2	478	8	ADP31007	Adp31007 Human sec
20	46	85.2	828	8	ADP30878	Adp30878 Human sec
21	46	85.2	921	10	AEI57577	Aei57577 Thale cre
22	46	85.2	948	10	AEI57069	Aei57069 Thale cre
23	46	85.2	1134	8	ADP30924	Adp30924 Human sec
24	46	85.2	1182	10	AEI55675	Aei55675 Thale cre
25	46	85.2	1195	10	AEI57953	Aei57953 Thale cre
26	46	85.2	1199	10	AEI55925	Aei55925 Thale cre
27	46	85.2	1221	10	AEI56793	Aei56793 Zea mays
28	46	85.2	1337	10	AEI56429	Aei56429 Zea mays
29	46	85.2	1469	10	AEI57423	Aei57423 Thale cre
30	46	85.2	1470	10	AEI56813	Aei56813 Thale cre
31	46	85.2	2148	10	AEI57533	Aei57533 Thale cre
32	45	83.3	588	8	ADP31699	Adp31699 Human sec
33	45	83.3	645	10	AEI57601	Aei57601 Thale cre
34	45	83.3	1050	8	ADP31376	Adp31376 Human sec
35	45	83.3	1101	8	ADP31462	Adp31462 Human sec
36	45	83.3	1260	10	AEI57327	Aei57327 Thale cre
37	45	83.3	1407	10	AEI57031	Aei57031 Thale cre
38	45	83.3	1492	10	AEI58447	Aei58447 Soybean p
39	45	83.3	1530	10	AEI57395	Aei57395 Thale cre
40	45	83.3	1652	10	AEI56983	Aei56983 Thale cre
41	45	83.3	1743	6	ABU88255	Abu88255 Novel hum
42	45	83.3	1743	6	ABU90134	Abu90134 Novel hum
43	45	83.3	1743	6	ABU96436	Abu96436 Novel hum
44	45	83.3	1743	6	ABU99045	Abu99045 Novel hum
45	45	83.3	1743	6	ABU98260	Abu98260 Novel hum

ALIGNMENTS

RESULT 1  
AEI56561  
ID AEI56561 standard; protein; 1663 AA.  
XX  
AC AEI56561;  
XX  
DT 24-AUG-2006 (first entry)  
XX  
DE Thale cress polypeptide, SEQ ID NO: 1028.  
XX  
KW plant; transgenic plant; mapping.  
XX  
OS Arabidopsis thaliana.  
XX



# SCORE Search Results Details for Application 10539637 and Search Result 20070420\_155801\_us-10-539-637-5.rag.

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OM protein - protein search, using sw model

Run on: April 21, 2007, 06:24:28 ; Search time 64 Seconds  
(without alignments)  
251.370 Million cell updates/sec

Title: US-10-539-637-5  
Perfect score: 54  
Sequence: 1 CXXXXXXXXXXXXCXXXCXXXXXXXXXXXXXXXXX 33

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2782304 seqs, 489333398 residues

Total number of hits satisfying chosen parameters: 2782304

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_200701:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*  
9: geneseqp2005s:\*  
10: geneseqp2006s:\*  
11: geneseqp2007s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
------------	-------	---------	--------------	-------	-------------

1	49	90.7	774	8	ADP30780	Adp30780 Human sec
2	49	90.7	774	8	ADP30781	Adp30781 Human sec
3	49	90.7	1209	8	ADP30782	Adp30782 Human sec
4	49	90.7	1757	10	AEI56087	Aei56087 Zea mays
5	49	90.7	10944	8	ADP31311	Adp31311 Human sec
6	49	90.7	11328	8	ADP31310	Adp31310 Human sec
7	48	88.9	1033	8	ADP30984	Adp30984 Human sec
8	48	88.9	1383	10	AEI57315	Aei57315 Thale cre
9	48	88.9	1505	10	AEI57155	Aei57155 Thale cre
10	48	88.9	1865	10	AEI56611	Aei56611 Zea mays
11	48	88.9	1884	10	AEI58121	Aei58121 Thale cre
12	48	88.9	1934	10	AEI57275	Aei57275 Thale cre
13	48	88.9	2077	10	AEI57873	Aei57873 Thale cre
14	48	88.9	2337	10	AEI57401	Aei57401 Thale cre
15	47	87.0	984	10	AEI57555	Aei57555 Thale cre
16	47	87.0	1056	10	AEI57309	Aei57309 Thale cre
17	47	87.0	1353	10	AEI57035	Aei57035 Thale cre
18	47	87.0	1383	8	ADP31091	Adp31091 Human sec
19	47	87.0	1510	10	AEI56117	Aei56117 Zea mays
20	47	87.0	1581	10	AEI56847	Aei56847 Thale cre
21	47	87.0	1602	9	ADZ66459	Adz66459 Human ARN
22	47	87.0	7339	6	AAO16358	Aao16358 Human tra
23	46	85.2	588	8	ADP31699	Adp31699 Human sec
24	46	85.2	699	8	ADP31080	Adp31080 Human sec
25	46	85.2	699	8	ADP31079	Adp31079 Human sec
26	46	85.2	762	8	ADP30891	Adp30891 Human sec
27	46	85.2	1038	10	AEI55751	Aei55751 Thale cre
28	46	85.2	1053	10	AEI56763	Aei56763 Zea mays
29	46	85.2	1077	10	AEI57463	Aei57463 Thale cre
30	46	85.2	1205	10	AEI58291	Aei58291 Thale cre
31	46	85.2	1253	10	AEI58123	Aei58123 Thale cre
32	46	85.2	1254	10	AEI56373	Aei56373 Thale cre
33	46	85.2	1337	10	AEI56893	Aei56893 Thale cre
34	46	85.2	1395	10	AEI58157	Aei58157 Thale cre
35	46	85.2	1396	10	AEI55899	Aei55899 Thale cre
36	46	85.2	1462	10	AEI58775	Aei58775 Bread whe
37	46	85.2	1478	10	AEI57009	Aei57009 Thale cre
38	46	85.2	1581	10	AEI57407	Aei57407 Thale cre
39	46	85.2	1637	10	AEI58095	Aei58095 Thale cre
40	46	85.2	1637	10	AEI57711	Aei57711 Thale cre
41	46	85.2	1783	10	AEI56973	Aei56973 Thale cre
42	46	85.2	1919	10	AEI57703	Aei57703 Zea mays
43	46	85.2	2016	10	AEI57721	Aei57721 Zea mays
44	46	85.2	2016	10	AEI56885	Aei56885 Thale cre
45	46	85.2	2068	10	AEI58195	Aei58195 Thale cre

## ALIGNMENTS

## RESULT 1

## ADP30780

ID ADP30780 standard; protein; 774 AA.

XX

AC ADP30780;

XX

DT 01-DEC-2005 (revised)

DT 12-AUG-2004 (first entry)

XX

DE Human secreted protein SEQ ID #2778.

XX

KW Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide;

KW cancer; inflammatory; immune; human secreted protein.

XX

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1.rup.

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OM protein - protein search, using sw model

Run on: April 21, 2007, 06:27:45 ; Search time 329 Seconds  
(without alignments)  
410.776 Million cell updates/sec

Title: US-10-539-637-1  
Perfect score: 54  
Sequence: 1 CXXXXXXXXXXXXXXXXXXXXX.....XXXXXXXXXXXXXXXXXXXXX 126

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 3281787 seqs, 1072124677 residues

Total number of hits satisfying chosen parameters: 3281787

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_8.4:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query Match	Length			
1	28	51.9	269	2	Q7PRQ7_ANOGA	Q7prq7 anopheles g
2	25	46.3	881	2	Q8IMS9_DROME	Q8ims9 drosophila
3	15	27.8	117	2	Q5K0Z7_DROSU	Q5k0z7 drosophila
4	15	27.8	117	2	Q5K0Z8_DROSU	Q5k0z8 drosophila
5	15	27.8	117	2	Q5K0X1_DROMD	Q5k0x1 drosophila
6	15	27.8	117	2	Q5K0Y9_DROSU	Q5k0y9 drosophila
7	15	27.8	117	2	Q5K0Z1_DROSU	Q5k0z1 drosophila
8	15	27.8	117	2	Q5K0Y8_DROSU	Q5k0y8 drosophila

9	15	27.8	117	2	Q5K0Z4_DROSU	Q5k0z4 drosophila
10	15	27.8	188	2	Q86HD2_DICDI	Q86hd2 dictyosteli
11	15	27.8	207	2	Q551N1_DICDI	Q551n1 dictyosteli
12	15	27.8	328	2	Q6H731_ORYSA	Q6h731 oryza sativ
13	15	27.8	1514	2	Q1H9R3_9FILI	Q1h9r3 cyathea arb
14	15	27.8	1873	2	Q4QIR9_LEIMA	Q4qir9 leishmania
15	14	25.9	97	2	Q6ESY9_ORYSA	Q6esy9 oryza sativ
16	14	25.9	117	2	Q5K0X7_DROSU	Q5k0x7 drosophila
17	14	25.9	117	2	Q5K0X9_DROSU	Q5k0x9 drosophila
18	14	25.9	117	2	Q5K0Y5_DROSU	Q5k0y5 drosophila
19	14	25.9	117	2	Q5K0Y3_DROSU	Q5k0y3 drosophila
20	14	25.9	117	2	Q5K0Y4_DROSU	Q5k0y4 drosophila
21	14	25.9	117	2	Q5K0Y1_DROSU	Q5k0y1 drosophila
22	14	25.9	731	2	Q25AD0_ORYSA	Q25ad0 oryza sativ
23	14	25.9	731	2	Q7XXF5_ORYSA	Q7xxf5 oryza sativ
24	14	25.9	778	2	Q3U2K0_MOUSE	Q3u2k0 mus musculu
25	14	25.9	834	2	Q69Z63_MOUSE	Q69z63 mus musculu
26	14	25.9	999	1	SMG_DROME	Q23972 drosophila
27	14	25.9	3893	2	Q4P6L1_USTMA	Q4p6l1 ustilago ma
28	13	24.1	137	2	Q6BES2_CAEEL	Q6bes2 caenorhabdi
29	13	24.1	141	2	Q84MF8_ORYSA	Q84mf8 oryza sativ
30	13	24.1	222	2	Q5M951_RAT	Q5m951 rattus norv
31	13	24.1	274	2	Q9M7I5_MAIZE	Q9m7i5 zea mays (m
32	13	24.1	1426	2	Q2XXS7_DROYA	Q2xxs7 drosophila
33	13	24.1	2374	2	Q4Q9W7_LEIMA	Q4q9w7 leishmania
34	12	22.2	71	2	Q8VB36_WSSV	Q8vb36 white spot
35	12	22.2	145	2	Q60LP6_CAEBR	Q60lp6 caenorhabdi
36	12	22.2	156	2	O16422_CAEEL	O16422 caenorhabdi
37	12	22.2	170	2	Q6QLW6_PECGU	Q6qlw6 pectinaria
38	12	22.2	172	2	Q18827_CAEEL	Q18827 caenorhabdi
39	12	22.2	210	2	Q8S421_MAIZE	Q8s421 zea mays (m
40	12	22.2	240	2	Q9GYJ4_CAEEL	Q9gyj4 caenorhabdi
41	12	22.2	257	2	Q9XV90_CAEEL	Q9xv90 caenorhabdi
42	12	22.2	269	2	Q7SG56_NEUCR	Q7sg56 neurospora
43	12	22.2	285	2	Q86K16_DICDI	Q86k16 dictyosteli
44	12	22.2	285	2	Q556P2_DICDI	Q556p2 dictyosteli
45	12	22.2	297	2	Q9VN10_DROME	Q9vn10 drosophila

## ALIGNMENTS

## RESULT 1

## Q7PRQ7\_ANOGA

ID Q7PRQ7\_ANOGA PRELIMINARY; PRT; 269 AA.  
AC Q7PRQ7;  
DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.  
DT 07-DEC-2004, sequence version 2.  
DT 07-FEB-2006, entry version 10.  
DE ENSANGP00000001657 (Fragment).  
GN ORFNames=ENSANGG000000001387;  
OS Anopheles gambiae str. PEST.  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;  
OC Anophelinae; Anopheles.  
OX NCBI\_TaxID=180454;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=PEST;  
RG The Anopheles gambiae Sequence Committee;  
RT "Anopheles gambiae re-annotation."  
RL Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=PEST;

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2.rup.

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OM protein - protein search, using sw model

Run on: April 21, 2007, 06:27:45 ; Search time 172 Seconds  
(without alignments)  
410.776 Million cell updates/sec

Title: US-10-539-637-2  
Perfect score: 54  
Sequence: 1 CXXXXXXXXXXCXXXXXXXXX.....XXXXXXXXXXCXXXXXXXXXXX 66

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 3281787 seqs, 1072124677 residues

Total number of hits satisfying chosen parameters: 3281787

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_8.4:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

°

SUMMARIES						
		%				
		Query				
Result No.	Score	Match	Length	DB	ID	Description
1	34	63.0	191	2	Q4MSA1_BACCE	Q4msa1 bacillus ce
2	31	57.4	2087	2	Q4S488_TETNG	Q4s488 tetraodon n
3	24	44.4	284	2	Q4TC48_TETNG	Q4tc48 tetraodon n
4	23	42.6	245	2	O18039_CAEL	O18039 caenorhabdi
5	23	42.6	481	2	Q19PM1_POPTR	Q19pm1 populus tri
6	20	37.0	183	2	Q8S3W8_HORVD	Q8s3w8 hordeum vul
7	20	37.0	638	2	Q41M45_METBU	Q41m45 methanococc
8	19.5	36.1	1514	2	Q1H9R3_9FILI	Q1h9r3 cyathea arb

9	19	35.2	212	2	Q26K76_XANP2	Q26k76 xanthobacte
10	19	35.2	360	2	Q2R9V7_ORYSA	Q2r9v7 oryza sativ
11	19	35.2	370	2	Q5SPC8_BRARE	Q5spc8 brachydanio
12	19	35.2	372	2	Q5SPC7_BRARE	Q5spc7 brachydanio
13	19	35.2	574	2	Q4P0R6_USTMA	Q4p0r6 ustilago ma
14	19	35.2	673	2	Q8I0P4_GIALA	Q8i0p4 giardia lam
15	19	35.2	1107	2	Q5CV70_CRYPV	Q5cv70 cryptospori
16	19	35.2	1225	2	Q4S5A8_TETNG	Q4s5a8 tetraodon n
17	19	35.2	2756	2	Q8IE61_PLAF7	Q8ie61 plasmodium
18	18	33.3	91	2	Q4XC49_PLACH	Q4xc49 plasmodium
19	18	33.3	158	2	Q2XNT8_ASPOF	Q2xnt8 asparagus o
20	18	33.3	307	1	SGS3_DROME	P02840 drosophila
21	18	33.3	312	2	Q5RJ00_BRARE	Q5rj00 brachydanio
22	18	33.3	314	2	Q5RIZ9_BRARE	Q5riz9 brachydanio
23	18	33.3	347	2	Q8K340_MOUSE	Q8k340 mus musculu
24	18	33.3	362	2	Q8C0D3_MOUSE	Q8c0d3 mus musculu
25	18	33.3	367	2	Q6AV38_ORYSA	Q6av38 oryza sativ
26	18	33.3	584	2	Q8BL43_MOUSE	Q8bl43 m adult mal
27	18	33.3	593	2	O10288_NPVOP	O10288 orgyia pseu
28	18	33.3	730	2	Q8LP13_PEA	Q8lp13 pisum sativ
29	18	33.3	1464	2	Q1DK15_COCIM	Q1dk15 coccidioide
30	17	31.5	35	2	Q9LQI2_ARATH	Q9lqi2 arabidopsis
31	17	31.5	86	2	Q9YY33_9HIV1	Q9yy33 human immun
32	17	31.5	93	2	Q6EUA6_ORYSA	Q6eua6 oryza sativ
33	17	31.5	137	2	Q24960_GIALA	Q24960 giardia lam
34	17	31.5	137	2	Q24987_GIALA	Q24987 giardia lam
35	17	31.5	144	2	Q1HQL0_AEDAE	Q1hql0 aedes aegyp
36	17	31.5	146	2	Q1HQB9_AEDAE	Q1hqb9 aedes aegyp
37	17	31.5	155	2	Q6Y1L9_DROYA	Q6y1l9 drosophila
38	17	31.5	155	2	Q7Z1J0_DROSI	Q7z1j0 drosophila
39	17	31.5	155	2	Q7YSR5_DROME	Q7ysr5 drosophila
40	17	31.5	210	2	Q7XHS1_ORYSA	Q7xhs1 oryza sativ
41	17	31.5	234	2	Q9XY90_GIALA	Q9xy90 giardia lam
42	17	31.5	259	2	Q5C550_SCHJA	Q5c550 schistosoma
43	17	31.5	269	2	Q7PRQ7_ANOGA	Q7prq7 anopheles g
44	17	31.5	293	2	Q66IW1_XENLA	Q66iw1 xenopus lae
45	17	31.5	294	2	Q9XUS0_CAEEL	Q9xus0 caenorhabdi

## ALIGNMENTS

## RESULT 1

## Q4MSA1\_BACCE

ID Q4MSA1\_BACCE PRELIMINARY; PRT; 191 AA.

AC Q4MSA1;

DT 02-AUG-2005, integrated into UniProtKB/TrEMBL.

DT 02-AUG-2005, sequence version 1.

DT 07-FEB-2006, entry version 2.

DE Hypothetical protein.

GN ORFNames=BCE\_G9241\_1290;

OS Bacillus cereus G9241.

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;

OC Bacillus cereus group.

OX NCBI\_TaxID=269801;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=G9241;

RX PubMed=15155910; DOI=10.1073/pnas.0402414101;

RA Hoffmaster A.R., Ravel J., Rasko D.A., Chapman G.D., Chute M.D.,

RA Marston C.K., De B.K., Sacchi C.T., Fitzgerald C., Mayer L.W.,

RA Maiden M.C.J., Priest F.G., Barker M., Jiang L., Cer R.Z.,

RA Rilstone J., Peterson S.N., Weyant R.S., Galloway D.R., Read T.D.,

RA Popovic T., Fraser C.M.;

RT "Identification of anthrax toxin genes in a Bacillus cereus associated

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3.rup.

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OM protein - protein search, using sw model

Run on: April 21, 2007, 06:27:45 ; Search time 110 Seconds  
(without alignments)  
410.776 Million cell updates/sec

Title: US-10-539-637-3  
Perfect score: 54  
Sequence: 1 CXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX 42

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 3281787 seqs, 1072124677 residues

Total number of hits satisfying chosen parameters: 3281787

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_8.4:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%						
Result		Query						
No.	Score	Match	Length	DB	ID		Description	
1	34.5	63.9	1514	2	Q1H9R3_9FILI		Q1h9r3 cyathea arb	
2	33.5	62.0	269	2	Q7PRQ7_ANOGA		Q7prq7 anopheles g	
3	31.5	58.3	69	2	Q9NCS8_CONEA		Q9ncs8 conus ebrae	
4	31.5	58.3	69	2	Q9NCS9_CONEA		Q9ncs9 conus ebrae	
5	31.5	58.3	69	2	Q9NCT3_CONEA		Q9nct3 conus ebrae	
6	31.5	58.3	69	2	Q9NCT2_CONEA		Q9nct2 conus ebrae	
7	31.5	58.3	69	2	Q9N669_CONEA		Q9n669 conus ebrae	
8	31	57.4	91	2	Q4XC49_PLACH		Q4xc49 plasmodium	

9	31	57.4	644	2	Q2IKE0_ANADE	Q2ike0 anaeromyxob
10	30.5	56.5	69	2	Q9NCT0_CONEA	Q9nct0 conus ebrae
11	30.5	56.5	258	2	Q6BG33_PARTE	Q6bg33 paramecium
12	30	55.6	252	2	Q3SDA0_PARTE	Q3sda0 paramecium
13	30	55.6	1066	2	Q3H4T8_9ACTO	Q3h4t8 nocardioide
14	29.5	54.6	51	2	Q80LL0_NPVAH	Q80l10 adoxophyes
15	29.5	54.6	69	2	Q9NCT1_CONEA	Q9nct1 conus ebrae
16	29.5	54.6	69	2	Q9NCT4_CONEA	Q9nct4 conus ebrae
17	29.5	54.6	69	2	Q9NCT5_CONEA	Q9nct5 conus ebrae
18	29.5	54.6	69	2	Q9NCT7_CONEA	Q9nct7 conus ebrae
19	29.5	54.6	69	2	Q9NCT8_CONEA	Q9nct8 conus ebrae
20	29.5	54.6	69	2	Q9NCT6_CONEA	Q9nct6 conus ebrae
21	29.5	54.6	69	2	Q9NCU0_CONEA	Q9ncu0 conus ebrae
22	29.5	54.6	69	2	Q9N6A4_CONEA	Q9n6a4 conus ebrae
23	29.5	54.6	363	2	Q170Q5_AEDAE	Q170q5 aedes aegyp
24	29.5	54.6	705	2	Q2ILJ6_ANADE	Q2ilj6 anaeromyxob
25	29	53.7	65	1	MT_PARLI	P80367 paracentrot
26	29	53.7	66	1	MT_ARIAR	P55946 arianta arb
27	29	53.7	66	2	Q966Z5_PARLI	Q966z5 paracentrot
28	29	53.7	189	2	Q2VJJ7_DROAR	Q2vjj7 drosophila
29	29	53.7	189	2	Q2VJJ6_DROAR	Q2vjj6 drosophila
30	29	53.7	189	2	Q2VJJ8_DROAR	Q2vjj8 drosophila
31	29	53.7	318	2	Q41794_MAIZE	Q41794 zea mays (m
32	29	53.7	481	2	Q7UFT6_RHOBA	Q7uft6 rhodopirell
33	29	53.7	1350	2	Q1S7S0_MEDTR	Q1s7s0 medicago tr
34	28.5	52.8	50	2	Q8JM47_9NUCL	Q8jm47 mamestra co
35	28.5	52.8	50	2	Q8QLC7_9NUCL	Q8qlc7 mamestra co
36	28.5	52.8	52	1	CXOL2_NPVOP	O10286 orgyia pseu
37	28.5	52.8	52	2	Q9PYR8_GVXN	Q9pyr8 xestia c-ni
38	28.5	52.8	53	2	Q2NP33_NPVHC	Q2np33 hyphantria
39	28.5	52.8	71	2	Q9UA90_CONAB	Q9ua90 conus abbre
40	28.5	52.8	71	2	Q9UA87_CONAB	Q9ua87 conus abbre
41	28.5	52.8	71	2	Q9UA88_CONAB	Q9ua88 conus abbre
42	28.5	52.8	71	2	Q9TVX4_CONAB	Q9tvx4 conus abbre
43	28.5	52.8	279	2	Q170Q6_AEDAE	Q170q6 aedes aegyp
44	28.5	52.8	335	2	Q5BN34_ANOGA	Q5bn34 anopheles g
45	28.5	52.8	496	2	Q2IMT2_ANADE	Q2imt2 anaeromyxob

## ALIGNMENTS

## RESULT 1

## Q1H9R3\_9FILI

ID Q1H9R3\_9FILI PRELIMINARY; PRT; 1514 AA.  
AC Q1H9R3;  
DT 27-JUN-2006, integrated into UniProtKB/TrEMBL.  
DT 27-JUN-2006, sequence version 1.  
DT 27-JUN-2006, entry version 1.  
DE Putative alpha subunit of ATP synthase (Fragment).  
GN Name=atpA;  
OS Cyathea arborea.  
OG Plastid; Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Moniliformopses; Filicophyta; Filicopsida; Filicales; Cyatheaceae;  
OC Cyathea.  
OX NCBI\_TaxID=361543;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=16481203; DOI=10.1016/j.ympev.2006.01.001;  
RA Korall P., Pryer K.M., Metzgar J.S., Schneider H., Conant D.S.;  
RT "Tree ferns: Monophyletic groups and their relationships as revealed  
RT by four protein-coding plastid loci."  
RL Mol. Phylogenet. Evol. 39:830-845(2006).  
CC -----



SCORE Search Results Details for Application 10539637  
and Search Result 20070420\_155803\_us-10-539-637-  
4.rup.

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OM protein - protein search, using sw model

Run on: April 21, 2007, 06:27:45 ; Search time 86 Seconds  
(without alignments)  
410.776 Million cell updates/sec

Title: US-10-539-637-4  
Perfect score: 54  
Sequence: 1 CXXXCXXXXCXXXXXXXXXCXXXXXXXXXXXXXXXXX 33

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 3281787 seqs, 1072124677 residues

Total number of hits satisfying chosen parameters: 3281787

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_8.4:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%		Query			Description
Result No.	Score	Match	Length	DB	ID		
1	39	72.2	1514	2	Q1H9R3_9FILI	Q1h9r3 cyathea arb	
2	38	70.4	182	1	KRUC_SHEEP	P26372 ovis aries	
3	38	70.4	191	2	Q28583_SHEEP	Q28583 ovis aries	
4	35	64.8	30	1	CY01_VIOOD	P82230 viola odora	
5	35	64.8	30	1	HYPAA_HYBPA	P58445 hybanthus p	
6	35	64.8	63	1	IBB1_AMBAC	P83284 amburana ac	
7	35	64.8	63	1	IBB2_AMBCE	P83283 amburana ce	
8	35	64.8	76	1	IBB3_DOLAX	P01057 dolichos ax	

9	35	64.8	76	1	IBB_DOLBI	Q9s9e3	d horsegram
10	35	64.8	78	2	Q9S9H8_VIGUN	Q9s9h8	vigna ungui
11	35	64.8	82	1	IBB1_PHAAN	P01058	phaseolus a
12	35	64.8	83	1	IBB_VIGUN	P17734	vigna ungui
13	35	64.8	103	2	Q941H6_DOLBI	Q941h6	dolichos bi
14	35	64.8	104	2	Q941H5_VIGMU	Q941h5	vigna mungo
15	35	64.8	113	2	Q1W3Z5_VIGMU	Q1w3z5	vigna mungo
16	34.5	63.9	463	2	Q5PAM5_ANAMM	Q5pam5	anaplasma m
17	34.5	63.9	485	2	Q5PAG9_ANAMM	Q5pag9	anaplasma m
18	34.5	63.9	532	2	Q5PAM7_ANAMM	Q5pam7	anaplasma m
19	34	63.0	30	1	VHR1_VIOHE	P83937	viola heder
20	34	63.0	31	1	CYLA_PSYLO	P56872	psychotria
21	34	63.0	31	1	HYFLA_HYBFL	P84647	hybanthus f
22	34	63.0	33	2	Q30CA1_9ROSI	Q30ca1	hybanthus e
23	34	63.0	41	2	Q39806_SOYBN	Q39806	glycine max
24	34	63.0	67	1	IBB1_DIOGL	P82469	dioclea gla
25	34	63.0	76	1	IBB4_DOLAX	P01059	dolichos ax
26	34	63.0	80	1	IBB4_LONCA	P16343	lonchocarpu
27	34	63.0	83	1	IBB_PHALU	P01056	phaseolus l
28	34	63.0	104	2	Q941H3_PHALU	Q941h3	phaseolus l
29	34	63.0	107	2	Q84X88_VIGSI	Q84x88	vigna sinen
30	34	63.0	110	1	IBB1_SOYBN	P01055	glycine max
31	34	63.0	110	2	Q53ZY0_SOYBN	Q53zy0	glycine max
32	34	63.0	111	2	Q84LF5_9FABA	Q84lf5	glycine mic
33	34	63.0	112	2	Q1W3Z3_9FABA	Q1w3z3	vigna marin
34	34	63.0	118	2	Q8RU23_GLYSO	Q8ru23	glycine soj
35	34	63.0	118	2	Q8RU24_GLYSO	Q8ru24	glycine soj
36	34	63.0	361	2	Q16VZ1_AEDAE	Q16vz1	aedes aegyp
37	33	61.1	30	1	CYO7_VIOOD	P58439	viola odora
38	33	61.1	42	1	CXS3A_CONGE	P58924	conus geogr
39	33	61.1	60	2	Q29Y80_LENCU	Q29y80	lens culina
40	33	61.1	61	1	IBB_ERYVA	P81705	erythrina v
41	33	61.1	72	1	IBB_PHAAU	P01062	phaseolus a
42	33	61.1	75	2	Q7M1Q0_CANLI	Q7m1q0	canavalia l
43	33	61.1	76	2	Q7M1P9_CANLI	Q7m1p9	canavalia l
44	33	61.1	78	1	IBB2_PHAAN	P01061	phaseolus a
45	33	61.1	79	1	IBB2_PHAVU	P01060	phaseolus v

## ALIGNMENTS

## RESULT 1

## Q1H9R3\_9FILI

ID Q1H9R3\_9FILI PRELIMINARY; PRT; 1514 AA.

AC Q1H9R3;

DT 27-JUN-2006, integrated into UniProtKB/TrEMBL.

DT 27-JUN-2006, sequence version 1.

DT 27-JUN-2006, entry version 1.

DE Putative alpha subunit of ATP synthase (Fragment).

GN Name=atpA;

OS Cyathea arborea.

OG Plastid; Chloroplast.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Moniliformopses; Filicophyta; Filicopsida; Filicales; Cyatheaceae;

OC Cyathea.

OX NCBI\_TaxID=361543;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RX PubMed=16481203; DOI=10.1016/j.ympev.2006.01.001;

RA Korall P., Pryer K.M., Metzgar J.S., Schneider H., Conant D.S.;

RT "Tree ferns: Monophyletic groups and their relationships as revealed

RT by four protein-coding plastid loci.";

RL Mol. Phylogenet. Evol. 39:830-845(2006).

CC -----

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5.rup.

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OM protein - protein search, using sw model

Run on: April 21, 2007, 06:27:45 ; Search time 86 Seconds  
(without alignments)  
410.776 Million cell updates/sec

Title: US-10-539-637-5  
Perfect score: 54  
Sequence: 1 CXXXXXXXXXXXXCXXXCXXXXXXXXXXXXXXXXX 33

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 3281787 seqs, 1072124677 residues

Total number of hits satisfying chosen parameters: 3281787

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_8.4:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES						
%						
Result	Query					
No.	Score	Match	Length	DB	ID	Description
1	39	72.2	73	2	Q5K4A7_9BIVA	Q5k4a7 bathymodiol
2	38	70.4	72	1	MT13_MYTED	P80248 mytilus edu
3	38	70.4	72	1	MT14_MYTED	P80249 mytilus edu
4	38	70.4	73	2	Q697L7_MYTGA	Q697l7 mytilus gal
5	38	70.4	73	2	Q70JU6_MYTED	Q70ju6 mytilus edu
6	38	70.4	73	2	Q5K4A9_9BIVA	Q5k4a9 bathymodiol
7	38	70.4	426	2	Q67UU9_ORYSA	Q67uu9 oryza sativ
8	37	68.5	42	1	CXS3A_CONGE	P58924 conus geogr

9	37	68.5	72	1	MT12_MYTED	P80247	mytilus edu
10	37	68.5	223	2	Q18DU6_9EURY	Q18du6	haloquadrat
11	36	66.7	31	2	Q1WW94_DROME	Q1ww94	drosophila
12	36	66.7	44	1	MT4_DROME	Q8i9b4	drosophila
13	36	66.7	45	1	MT54_BRANA	P43402	brassica na
14	36	66.7	45	2	Q71M48_BRAOL	Q71m48	brassica ol
15	36	66.7	62	2	Q6VQN8_CRAVI	Q6vqn8	crassostrea
16	36	66.7	62	2	Q6VQN9_CRAVI	Q6vqn9	crassostrea
17	36	66.7	62	2	Q8MUZ6_CRAVI	Q8muz6	crassostrea
18	36	66.7	70	2	Q967T9_9BIVA	Q967t9	tegillarca
19	36	66.7	72	1	MT10A_MYTED	P80246	mytilus edu
20	36	66.7	72	1	MT10B_MYTED	O62554	mytilus edu
21	35	64.8	41	2	Q52P91_ANOGA	Q52p91	anopheles g
22	35	64.8	45	1	MT1C_ARATH	Q38804	arabidopsis
23	35	64.8	45	2	Q9M698_BRAOL	Q9m698	brassica ol
24	35	64.8	64	1	MTCU_CALSI	Q9u620	callinectes
25	35	64.8	74	1	MT_CRAVI	P23038	crassostrea
26	35	64.8	75	2	Q6VQP8_CRAVI	Q6vqp8	crassostrea
27	35	64.8	75	2	Q53ZD1_CRAVI	Q53zd1	crassostrea
28	35	64.8	76	2	Q19Q30_9DIPT	Q19q30	belgica ant
29	35	64.8	352	2	Q969V5_HUMAN	Q969v5	homo sapien
30	35	64.8	352	2	Q7Z431_HUMAN	Q7z431	homo sapien
31	35	64.8	352	2	Q9H9B5_HUMAN	Q9h9b5	homo sapien
32	35	64.8	352	2	Q4R7G8_MACFA	Q4r7g8	macaca fasc
33	35	64.8	353	2	Q6NTT6_XENLA	Q6ntt6	xenopus lae
34	35	64.8	922	2	Q389B2_9TRYP	Q389b2	trypanosoma
35	35	64.8	1477	2	Q8BYW0_MOUSE	Q8byw0	mus musculu
36	35	64.8	1514	2	Q1H9R3_9FILI	Q1h9r3	cyathea arb
37	35	64.8	2120	1	TECTA_CHICK	Q9yh85	gallus gall
38	35	64.8	2813	1	VWF_HUMAN	P04275	homo sapien
39	35	64.8	4782	2	Q8K1G6_MOUSE	Q8k1g6	mus musculu
40	35	64.8	5703	1	MUC5B_HUMAN	Q9hc84	homo sapien
41	35	64.8	23015	2	Q8IQ18_DROME	Q8iq18	drosophila
42	34	63.0	34	2	Q4YAQ7_PLABE	Q4yaq7	plasmodium
43	34	63.0	43	1	MT2_DROME	P11956	drosophila
44	34	63.0	43	2	Q1ECC1_DROME	Q1ecc1	drosophila
45	34	63.0	45	1	MT1A_ARATH	P43392	arabidopsis

ALIGNMENTS

RESULT 1  
Q5K4A7\_9BIVA  
ID Q5K4A7\_9BIVA PRELIMINARY; PRT; 73 AA.  
AC Q5K4A7;  
DT 15-FEB-2005, integrated into UniProtKB/TrEMBL.  
DT 15-FEB-2005, sequence version 1.  
DT 13-JUN-2006, entry version 7.  
DE Metallothionein, isoform MT-10c (Metallothionein, isoform MT- 10b).  
GN Name=MT-10c; Synonyms=MT-10b;  
OS Bathymodiolus azoricus.  
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Mytiloida;  
OC Mytiloidea; Mytilidae; Bathymodiolinae; Bathymodiolus.  
OX NCBI\_TaxID=150808;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Hardivillier Y.V., Leignel V.S., Denis F., Uguen G., Cosson R.,  
RA Laulier M.;  
RT "Do organisms living around hydrothermal vent sites contain specific  
RT metallothioneins? The case of the genus Bathymodiolus (Bivalvia,  
RT Mytilidae).";  
RL Comp. Biochem. Physiol. C, Comp. Pharmacol. Toxicol.  
RL 139:111-118(2004).  
CC -----

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OM protein - protein search, using sw model

Run on: April 21, 2007, 06:37:44 ; Search time 36 Seconds  
(without alignments)  
335.640 Million cell updates/sec

Title: US-10-539-637-1  
Perfect score: 54  
Sequence: 1 CXXXXXXXXXXXXXXXXXXXXX.....XXXXXXXXXXXXXXXXXXXXX 126

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_80:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	12	22.2	156	2	T31839	hypothetical prote
2	12	22.2	172	2	T20210	hypothetical prote
3	12	22.2	240	2	T25641	hypothetical prote
4	12	22.2	257	2	T21029	hypothetical prote
5	12	22.2	293	2	T31840	hypothetical prote
6	12	22.2	360	2	T09991	threonine synthase
7	12	22.2	360	2	C70773	threonine synthase
8	12	22.2	1533	2	A46221	abdominal segment
9	12	22.2	1788	2	T29043	hypothetical prote
10	11	20.4	97	2	T28947	hypothetical prote
11	11	20.4	259	2	T27783	hypothetical prote

12	11	20.4	352	2	A25364	threonine synthase
13	11	20.4	744	2	T20969	hypothetical prote
14	11	20.4	2176	2	T13806	toucan gene protei
15	10	18.5	130	2	A72553	hypothetical prote
16	10	18.5	352	1	DWFKTG	threonine synthase
17	10	18.5	354	2	E84077	threonine synthase
18	10	18.5	355	2	A34597	rhomboid protein -
19	10	18.5	405	2	H64482	threonine synthase
20	10	18.5	406	2	G69131	threonine synthase
21	10	18.5	2718	2	A23475	G surface protein
22	9	16.7	3	3	A22565	R-phycoerythrin al
23	9	16.7	4	2	I51049	metallothionein-A
24	9	16.7	4	2	S43959	Ig mu chain V regi
25	9	16.7	4	2	S55238	pallidipin - assas
26	9	16.7	5	2	B22565	R-phycoerythrin al
27	9	16.7	5	2	F22565	R-phycoerythrin ga
28	9	16.7	5	2	A33882	cadmium-binding pe
29	9	16.7	5	2	B45525	actin I - malaria
30	9	16.7	5	2	S65726	hemoglobin, extrac
31	9	16.7	6	2	JU0355	lipopeptide WS1279
32	9	16.7	6	2	C22565	R-phycoerythrin be
33	9	16.7	6	2	I37027	protamine P1 - gor
34	9	16.7	6	2	I37263	Y protein - human
35	9	16.7	6	2	H48394	glycoprotein compo
36	9	16.7	6	2	I67345	MHC H2-K-k cell su
37	9	16.7	6	2	I65546	MHC H2-L antigen -
38	9	16.7	6	2	PT0652	T-cell receptor be
39	9	16.7	6	2	F41946	T-cell receptor ga
40	9	16.7	6	2	I49421	laminin B1 - weste
41	9	16.7	6	2	S29881	Na+/K+-exchanging
42	9	16.7	6	4	I79564	hypothetical TCL3
43	9	16.7	7	2	PH1408	Ig heavy chain V r
44	9	16.7	7	2	S38516	mabinlin II chain
45	9	16.7	7	2	B34818	vicilin 57K chain

ALIGNMENTS

RESULT 1  
T31839  
hypothetical protein T05B4.13 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T31839  
R;Bradshaw, H.  
submitted to the EMBL Data Library, July 1997  
A;Description: The sequence of C. elegans cosmid T05B4.  
A;Reference number: Z21092  
A;Accession: T31839  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-156 <BRA>  
A;Cross-references: UNIPROT:O16422; UNIPARC:UPI000008086E; EMBL:AF016445; PIDN:AAC69061.1; GSPDB:GN  
A;Experimental source: strain Bristol N2; clone T05B4  
C;Genetics:  
A;Gene: CESP:T05B4.13  
A;Map position: 5  
A;Introns: 25/1

Query Match 22.2%; Score 12; DB 2; Length 156;  
Best Local Similarity 9.1%; Pred. No. 0;  
Matches 2; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

Qy 1 CXXXXXXXXXXXXXXXXXXXXC 22

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OM protein - protein search, using sw model

Run on: April 21, 2007, 06:37:44 ; Search time 19 Seconds  
(without alignments)  
335.640 Million cell updates/sec

Title: US-10-539-637-2  
Perfect score: 54  
Sequence: 1 CXXXXXXXXXXCXXXXXXXXX.....XXXXXXXXXXCXXXXXXXXXX 66

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_80:\*  
1: pirl:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		Match	Length	DB	ID	Description
	Score	Match					
1	23	42.6	245	2	T24565	hypothetical prote	
2	18	33.3	154	2	T08746	hypothetical prote	
3	18	33.3	247	2	T43136	hypothetical prote	
4	18	33.3	307	1	GSFF3	salivary glue prot	
5	18	33.3	593	2	T10301	ribonucleotide red	
6	17	31.5	294	2	T23682	hypothetical prote	
7	17	31.5	393	2	T41211	hypothetical wtf1	
8	17	31.5	418	2	T41027	hypothetical wtf5	
9	17	31.5	2703	1	A24420	notch protein - fr	
10	16.5	30.6	257	2	T21029	hypothetical prote	
11	16	29.6	152	2	D72630	hypothetical prote	

12	16	29.6	244	2	T31838	hypothetical prote
13	16	29.6	248	2	T31841	hypothetical prote
14	16	29.6	433	2	T50395	actin-related prot
15	16	29.6	539	2	T52565	glutathione syntha
16	16	29.6	596	2	T30498	probable ribonucle
17	16	29.6	667	2	A48579	trophozoite surfac
18	16	29.6	770	2	T51024	related to C2H2 zi
19	16	29.6	1041	2	T31097	chitin synthase (E
20	16	29.6	2610	2	T20968	hypothetical prote
21	16	29.6	4377	2	A55575	ankyrin 3, long sp
22	15.5	28.7	232	2	A60095	larval glue protei
23	15	27.8	98	2	E84599	hypothetical prote
24	15	27.8	154	2	AC0416	probable prepilin
25	15	27.8	166	2	F82774	hypothetical prote
26	15	27.8	226	2	B41378	cytochrome c553i p
27	15	27.8	248	2	T21786	hypothetical prote
28	15	27.8	268	2	A84746	probable NAM (no a
29	15	27.8	273	2	S69193	probable finger pr
30	15	27.8	283	2	AH2744	conserved hypothet
31	15	27.8	287	2	S57770	xyloglucan endo-1,
32	15	27.8	289	2	S49812	xyloglucan endo-1,
33	15	27.8	318	2	G97525	CG10208 protein (A
34	15	27.8	357	2	T21152	hypothetical prote
35	15	27.8	363	2	S18765	Sd protein - fruit
36	15	27.8	392	2	T27303	hypothetical prote
37	15	27.8	409	2	T08928	sucrose cleavage p
38	15	27.8	420	2	S74388	gamma-glutamyl pho
39	15	27.8	423	2	D96552	unknown protein, 7
40	15	27.8	503	2	S31126	hypothetical prote
41	15	27.8	569	2	B87180	pyruvate (or indol
42	15	27.8	727	2	JC7818	metalloproteinase
43	15	27.8	779	1	S40382	box A-binding fact
44	15	27.8	1003	1	PYVZAM	spheroidin precurs
45	15	27.8	1043	2	T19734	hypothetical prote

## ALIGNMENTS

RESULT 1  
T24565  
hypothetical protein T06C12.14 - *Caenorhabditis elegans*  
C;Species: *Caenorhabditis elegans*  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T24565  
R;Kelly, P.  
submitted to the EMBL Data Library, October 1996  
A;Reference number: Z19908  
A;Accession: T24565  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-245 <WIL>  
A;Cross-references: UNIPROT:O18039; UNIPARC:UPI000007C269; EMBL:Z81116; PIDN:CAB03300.1; GSPDB:GN0C  
A;Experimental source: clone T06C12  
C;Genetics:  
A;Gene: CESP:T06C12.14  
A;Map position: 5  
A;Introns: 33/3; 121/1  
C;Superfamily: *Caenorhabditis elegans* hypothetical protein C49G7.3

Query Match 42.6%; Score 23; DB 2; Length 245;  
Best Local Similarity 13.0%; Pred. No. 4e-19;  
Matches 3; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

Qy 1 CXXXXXXXXXXCXXXXXXXXXXC 23



SCORE Search Results Details for Application 10539637

10-539-637-3.r

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This page gives you Search Results detail for the Application 10539637 and Search Result 20070420\_155808\_us-

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OM protein - protein search, using sw model

Run on: April 21, 2007, 06:37:44 ; Search time 12 Seconds  
(without alignments)  
335.640 Million cell updates/sec

Title: US-10-539-637-3  
Perfect score: 54  
Sequence: 1 CXXXXXXXXXXXXXXXXXXXXXXX. ....XXXCXXXXXXXXXXXXXXXXXXXX 42

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_80:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES						
Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	29	53.7	66	2	S59621	metallothionein is
2	29	53.7	318	2	T03026	chitinase (EC 3.2.
3	28.5	52.8	52	2	T10299	conotoxin-like pro
4	28	51.9	182	2	A36686	ultra-high-sulfur
5	27	50.0	191	2	I46412	keratin KAP5.4 - s
6	27	50.0	613	2	S15468	complement C3b/C4b
7	27	50.0	1474	2	T18281	hypothetical prote
8	26.5	49.1	53	2	T10405	conotoxin-like pro
9	26.5	49.1	53	2	T30499	conotoxin-like pro

10	26	48.1	53	2	S24596	metallothionein -
11	26	48.1	61	2	S00810	metallothionein Ic
12	26	48.1	66	2	S36866	metallothionein -
13	26	48.1	67	2	T11547	metallothionein -
14	26	48.1	418	2	T29737	hypothetical prote
15	26	48.1	520	2	S47142	mating type A prot
16	26	48.1	654	2	T30136	hypothetical prote
17	26	48.1	671	2	AF0042	probable oxidoredu
18	25.5	47.2	53	2	C72850	conotoxin homolog
19	25.5	47.2	74	2	B59135	probable omega-con
20	25.5	47.2	442	2	T24196	hypothetical prote
21	25	46.3	61	1	SMHY1C	metallothionein I
22	25	46.3	61	1	SMMSI	metallothionein I
23	25	46.3	61	2	A37425	metallothionein 2
24	25	46.3	61	2	I54574	metallothionein-1
25	25	46.3	61	2	I46602	metallothionein -
26	25	46.3	62	2	S54336	metallothionein-2a
27	25	46.3	62	2	S54335	metallothionein-2c
28	25	46.3	62	2	I51538	metallothionein -
29	25	46.3	156	2	T31839	hypothetical prote
30	25	46.3	160	2	T25185	hypothetical prote
31	25	46.3	293	2	T31840	hypothetical prote
32	25	46.3	490	2	A45623	AnTat 11.17 varian
33	25	46.3	583	2	A29154	complement factor
34	25	46.3	1184	2	A55184	fibulin-2 precurso
35	25	46.3	1221	2	A49457	fibulin-2 precurso
36	25	46.3	2219	2	T27684	hypothetical prote
37	25	46.3	2533	2	T28675	alpha-51D immobili
38	25	46.3	2533	2	T28674	alpha-51D-immobili
39	25	46.3	2543	2	T31687	surface antigen - P
40	25	46.3	3175	1	RRWVEV	genome polyprotein
41	24.5	45.4	4660	2	T42737	gp330 protein prec
42	24	44.4	55	1	NTHNB2	neurotoxin B-II -
43	24	44.4	60	2	JC2419	metallothionein -
44	24	44.4	60	2	S31723	metallothionein -
45	24	44.4	60	2	B27490	metallothionein B

ALIGNMENTS

RESULT 1

S59621

metallothionein isoform b, cadmium-binding - Arianta arbustorum (terrestrial snail)

C;Species: Arianta arbustorum

C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 09-Jul-2004

C;Accession: S59621

R;Berger, B.; Hunziker, P.E.; Hauer, C.R.; Birchler, N.; Dallinger, R.

Biochem. J. 311, 951-957, 1995

A;Title: Mass spectrometry and amino acid sequencing of two cadmium-binding metallothionein isoform

A;Reference number: S59621; MUID:96067616; PMID:7487956

A;Accession: S59621

A;Molecule type: protein

A;Residues: 1-66 <BER>

A;Cross-references: UNIPROT:P55946; UNIPARC:UPI0000177CA1

C;Superfamily: metallothionein

C;Keywords: acetylated amino end; chelation; metal binding; metal-thiolate cluster

F;1/Modified site: acetylated amino end (Ser) #status experimental

Query Match53.7%; Score 29; DB 2; Length 66;

Best Local Similarity19.2%; Pred. No. 38;

Matches5; Conservative0; Mismatches21; Indels0; Gaps0;

Qy1 CXXXXXXXXXXXXXXXXXXXXC 26

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OM protein - protein search, using sw model

Run on: April 21, 2007, 06:37:44 ; Search time 9 Seconds  
(without alignments)  
335.640 Million cell updates/sec

Title: US-10-539-637-4  
Perfect score: 54  
Sequence: 1 CXXXCXXXCXXXXXXXXXCXXXXXXXXXXXXXXXXX 33

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_80:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		%					
Result		Query					
No.	Score	Match	Length	DB	ID	Description	
1	38	70.4	182	2	A36686	ultra-high-sulfur	
2	38	70.4	191	2	I46412	keratin KAP5.4 - s	
3	35	64.8	76	1	TIAM3	proteinase inhibit	
4	35	64.8	78	2	S09414	proteinase inhibit	
5	35	64.8	81	1	TI2B2	proteinase inhibit	
6	35	64.8	82	1	TI2B1	proteinase inhibit	
7	35	64.8	88	2	S09416	proteinase inhibit	
8	34	63.0	76	1	TIAM4	proteinase inhibit	
9	34	63.0	83	1	TILI	proteinase inhibit	
10	34	63.0	110	1	TISYO	proteinase inhibit	
11	33	61.1	41	2	A59149	sigma-conotoxin GV	

12	33	61.1	61	2	JX0309	proteinase inhibit
13	33	61.1	72	1	TIMB	trypsin inhibitor
14	33	61.1	72	1	TIZB1P	proteinase inhibit
15	33	61.1	73	2	JC1066	trypsin inhibitor
16	33	61.1	75	2	JC2072	double-headed prot
17	33	61.1	76	2	JC2073	double-headed prot
18	33	61.1	78	1	TIZB1A	proteinase inhibit
19	33	61.1	78	1	TIZB1B	proteinase inhibit
20	33	61.1	79	1	TIFB2	proteinase inhibit
21	33	61.1	83	2	S07405	proteinase inhibit
22	33	61.1	94	2	JC2225	Bowman-Birk protei
23	33	61.1	103	1	TISYC2	proteinase inhibit
24	33	61.1	146	2	S09415	proteinase inhibit
25	33	61.1	234	2	T30427	probable apoptosis
26	32	59.3	83	2	S07941	proteinase inhibit
27	32	59.3	96	2	S69007	trypsin/chymotryps
28	32	59.3	102	1	TISYD2	proteinase inhibit
29	32	59.3	113	2	S56647	trypsin inhibitor
30	32	59.3	113	2	S56648	trypsin inhibitor
31	32	59.3	114	2	S69006	trypsin/chymotryps
32	32	59.3	130	1	KRSH3A	keratin high-sulfu
33	32	59.3	131	1	KRGT3M	keratin high-sulfu
34	32	59.3	131	1	KRSHA3	keratin high-sulfu
35	32	59.3	132	1	KRGT3J	keratin high-sulfu
36	31	57.4	63	1	TIVF	proteinase inhibit
37	31	57.4	70	1	TINPA2	proteinase inhibit
38	31	57.4	223	2	B38346	ultra-high-sulfur
39	31	57.4	230	2	A38346	ultra-high-sulfur
40	30.5	56.5	459	2	I48854	gene murine tumour
41	30.5	56.5	474	2	B38634	tumor necrosis fac
42	30	55.6	53	2	S24596	metallothionein -
43	30	55.6	61	1	SMHU1B	metallothionein 1B
44	30	55.6	61	1	SMHY1C	metallothionein I
45	30	55.6	61	1	SMMSI	metallothionein I

ALIGNMENTS

RESULT 1  
A36686  
ultra-high-sulfur keratin - sheep  
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
C;Date: 12-Apr-1991 #sequence\_revision 12-Apr-1991 #text\_change 09-Jul-2004  
C;Accession: A36686  
R;MacKinnon, P.J.; Powell, B.C.; Rogers, G.E.  
J. Cell Biol. 111, 2587-2600, 1990  
A;Title: Structure and expression of genes for a class of cysteine-rich proteins of the cuticle lay  
A;Reference number: A36686; MUID:91115951; PMID:1703541  
A;Accession: A36686  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-182 <MAC>  
A;Cross-references: UNIPROT:P26372; UNIPARC:UPI000012E07B; GB:X55294; NID:g1305; PIDN:CAA39006.1; F  
C;Superfamily: ultra-high-sulfur keratin

Query Match 70.4%; Score 38; DB 2; Length 182;  
Best Local Similarity 23.1%; Pred. No. 12;  
Matches 6; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

Qy 1 CXXXCXXXCXXXXXXXXCXKXXXXXC 26  
| | | | |  
Db 148 CVPACSCSSCGKGGCGSCGCSQSSCC 173

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OM protein - protein search, using sw model

Run on: April 21, 2007, 06:37:44 ; Search time 9 Seconds  
(without alignments)  
335.640 Million cell updates/sec

Title: US-10-539-637-5  
Perfect score: 54  
Sequence: 1 CXXXXXXXXXXXXCXCXXXXXXXXXXXXXXXXX 33

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_80:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	38	70.4	72	2	S39418	metallothionein 10
2	38	70.4	72	2	S39419	metallothionein 10
3	37	68.5	41	2	A59149	sigma-conotoxin GV
4	37	68.5	72	2	S39417	metallothionein 10
5	36	66.7	72	2	S39416	metallothionein 10
6	35	64.8	45	2	S57860	metallothionein 1c
7	35	64.8	75	2	S17156	metallothionein -
8	35	64.8	1321	2	JE0352	mucin MUC5B, trach
9	35	64.8	2120	2	T30243	alpha tectorin - c
10	35	64.8	2813	1	VWHU	von Willebrand fac
11	34	63.0	43	1	SMFF2	metallothionein 2

12	34	63.0	45	2	S57858	metallothionein 1a
13	34	63.0	52	2	JC1197	metallothionein II
14	34	63.0	71	2	S39422	metallothionein 20
15	34	63.0	71	2	S39421	metallothionein 20
16	34	63.0	71	2	S47577	metallothionein 20
17	34	63.0	153	2	PN0564	von Willebrand fac
18	34	63.0	157	2	PN0563	von Willebrand fac
19	34	63.0	182	2	A36686	ultra-high-sulfur
20	34	63.0	223	2	B38346	ultra-high-sulfur
21	34	63.0	230	2	A38346	ultra-high-sulfur
22	33	61.1	27	2	T12330	metallothionein -
23	33	61.1	71	2	S47576	metallothionein 20
24	33	61.1	71	2	S39420	metallothionein 20
25	33	61.1	237	2	S08073	cyclic nucleotide
26	33	61.1	802	2	T24293	hypothetical prote
27	33	61.1	949	2	T24294	hypothetical prote
28	32	59.3	189	2	F89753	protein F11C7.5 [i
29	32	59.3	191	2	I46412	keratin KAP5.4 - s
30	32	59.3	454	2	T49171	hypothetical prote
31	32	59.3	1373	2	JE0095	gastric mucin MUC5
32	32	59.3	1620	2	T27283	hypothetical prote
33	31	57.4	57	2	S59073	metallothionein is
34	31	57.4	58	2	A37039	metallothionein 1
35	31	57.4	58	2	S43367	metallothionein -
36	31	57.4	58	2	S59072	metallothionein is
37	31	57.4	74	2	S57768	metallothionein-li
38	31	57.4	77	2	S30873	hypothetical prote
39	31	57.4	175	2	S37649	high-sulfur kerati
40	31	57.4	197	2	I46413	keratin KAP5.5 - s
41	31	57.4	233	2	A71336	hypothetical prote
42	31	57.4	404	2	T28114	hypothetical prote
43	31	57.4	407	2	T19895	hypothetical prote
44	31	57.4	863	2	C88546	protein R107.4 [im
45	31	57.4	1106	2	T18739	hypothetical prote

ALIGNMENTS

RESULT 1  
S39418  
metallothionein 10-III - blue mussel  
C;Species: Mytilus edulis (blue mussel)  
C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 09-Jul-2004  
C;Accession: S39418  
R;Mackay, E.A.; Overnell, J.; Dunbar, B.; Davidson, I.; Hunziker, P.E.; Kaegi, J.H.R.; Fothergill, Eur. J. Biochem. 218, 183-194, 1993  
A;Title: Complete amino acid sequences of five dimeric and four monomeric forms of metallothionein  
A;Reference number: S39416; MUID:94062828; PMID:8243463  
A;Accession: S39418  
A;Molecule type: protein  
A;Residues: 1-72 <MAC>  
A;Cross-references: UNIPROT:P80248; UNIPARC:UPI000012F6BD  
C;Superfamily: metallothionein  
C;Keywords: metal binding

Query Match 70.4%; Score 38; DB 2; Length 72;  
Best Local Similarity 24.0%; Pred. No. 13;  
Matches 6; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Qy 1 CXXXXXXXXXXXXCXXXCXXXXXC 25  
| | | | |  
Db 29 CKCSGADCKCSGCKVVCKCSGSCAC 53